SEQUENCE LISTING

<110> Garvan Institute of Medical Research <120> NPY-Y7 Receptor Gene <140> USSN 09/719,088 <141> 1999-06-29 <150> PP 4385 <151> 1998-06-29 <160> 5 <170> PatentIn Ver. 2.1 <210> 1 <211> 14 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: N-terminal consensus sequence <220> <221> misc-feature <222> (2)..(3)..(5)..(10) <223> Xaa = any codable amino acid <400> 1 Met Xaa Xaa Met Xaa Glu Lys Trp Asp Xaa Asn Ser Ser Glu 5 <210> 2 <211> 408 <212> PRT <213> Homo sapiens <400> 2 Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp 10 His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala

Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile 150 Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr 170 Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr 180 Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp 200 Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr 210 Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu 280 Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr 330 Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys

390

Ser Ala Glu Asn Pro Asn Arg Asn 405

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Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val 50 55 60

Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His 65 70 75 80

Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu 85 90 95

Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala 100 105 110

Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln
115 120 125

Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val 130 135 140

Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val 145 150 155 160

Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala 165 170 175

Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr 180 185 190

Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp 195 200 205

Cys Arg Glu Asp Trp Pro Arg His Glu Met Arg Arg Ile Tyr Thr Thr 210 215 220

Val Leu Phe Ala Ile Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile 225 230 235 240

Met Tyr Ala Arg Ile Gly Ala Ser Leu Phe Lys Thr Ala Ala His Cys 245 250 255

Thr Gly Lys Gln Arg Pro Val Gln Cys Met Tyr Gln Glu Lys Gln Lys 260 265 270

Val Ile Lys Met Leu Leu Thr Val Ala Leu Leu Phe Ile Leu Ser Trp 275 280 285

Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Thr Asp Leu Ser 290 295 300

Pro Asn Lys Leu Arg Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp Leu Ala Phe Cys Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe Asn Glu Asn Phe Arg Asn Gly Phe Cln Asp Ala Phe Gln Ite Cys Gln Lys Lys Ala Lys Pro Gln Glu Ala Tyr Ser Leu Arg Ala Lys Arg Asn Ile Val Ile Asn Thr Ser Gly Leu Leu Val Gln Glu Pro Val Ser Gln Asn Pro Gly Gly Glu Asn Leu Gly Cys Gly Lys Ser Ala Asp Asn 385 390 395 Pro His Arg Asn Pro <210> <211> 1903 <212> DNA <213> Homo sapiens <400> 4 ctcgagatcc attgtgctct aaaggcctcc tgagtagctg ggactacagg cgcccgccac 60 cacgcctggc taattttttt gtatttttag tagggacggc gtttcactgt gttagccaga 120 tggtctccat ctcccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180 caggogtgag accgogcog gocaatttoo tttottagtt gootetgooc acctottote 240 ttctgcttcc atattacagg tttcctcagt tgcgaaatta ggatgttaat tatagctttt 300 gacatacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgtagatcag 360 tgactgctat gttcatcatg aatgagaaat gggacacaaa ctcttcagaa aactggcatc 420 ccatctggaa tgtcaatgac acaaagcatc atctgtactc agatattaat attacctatg 480 tgaactacta tetteaceag ceteaagtgg cageaatett cattatttee taetttetga 540 tcttcttttt gtgcatgatg ggaaatactg tggtttgctt tattgtaatg aggaacaaac 600 atatgcacac agtcactaat ctcttcatct taaacctggc cataagtgat ttactagttg 660 gcatattctg catgcctata acactgctgg acaatattat agcaggatgg ccatttggaa 720 acacgatgtg caagatcagt ggattggtcc agggaatatc tgtcgcagct tcagtcttta 780 cgttagttgc aattgctgta gataggttcc agtgtgtggt ctaccctttt aaaccaaagc 840 tcactatcaa gacagcgttt gtcattatta tgatcatctg ggtcctagcc atcaccatta 900 tgtctccatc tgcagtaatg ttacatgtgc aagaagaaaa atattaccga gtgagactca 960 acteccagaa taaaaccagt ecagtetact ggtgeeggga agaetggeea aateaggaaa 1020 tgaggaagat ctacaccact gtgctgtttg ccaacatcta cctggctccc ctctccctca 1080 ttgtcatcat gtatggaagg attggaattt cactcttcag ggctgcagtt cctcacacag 1140 gcaggaagaa ccaggagcag tggcacgtgg tgtccaggaa gaagcagaag atcattaaga 1200 tgctcctgat tgtggccctg ctttttattc tctcatggct gcccctgtgg actctaatga 1260 tgctctcaga ctacgctgac ctttctccaa atgaactgca gatcatcaac atctacatct 1320 accettttge acactggetg geatteggea acageagtgt caateceate atttatggtt 1380 tetteaacga gaattteege egtggtttee aagaagettt ceageteeag etetgeeaaa 1440 aaagagcaaa gcctatggaa gcttataccc taaaagctaa aagccatgtg ctcataaaca 1500 catctaatca gcttgtccag gaatctacat ttcaaaaccc tcatggggaa accttgcttt 1560 ataggaaaag tgctgaaaac cccaacagga attagtgatg gaagaattaa aagaaactac 1620 taacagcagt gagatttaaa aagagctagt gtgataatcc taactctact acgcattata 1680 tatttaaatc cattgctttt tgtggctttg cacttcaaat ttttcaaaga atgttctaaa 1740 taaaacattt actgaaagcc ctctctggca aaaaaattaa aaataaacaa aaatggtcat 1800 aagatcataa acaatcttat gttgtataaa aatacgtaga gtgacttaga catgtttgca 1860

1903

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